

SEQUENCE LISTING

110> Boehringer Ingelheim International GmbH

<120> Method for Identifying Compounds Modulating Sister Chromatid Separation

<130> 0652.2290001 <140> US 10/051,311 <141> 2002-01-22 <150> US 60/297,440 <151> 2001-06-13 <150> EP 01 101 252.3 <151> 2001-01-19 <160> 13 <170> PatentIn Ver. 2.1 <210> 1 <211> 6668 <212> DNA <213> Homo sapiens <220> <221> 5'UTR <222> (1)..(144) <220> <221> CDS <222> (145)..(6507) <220> <221> 3'UTR <222> (6508)..(6668) <400> 1 tectggegtg ggttttetee eegatgaaat ttetgatgtg attetttgee teetteeacg 60 accttcagcc ctcttccctt cctccagtta gcttcattaa caatcttctc taattggtct 120 cetttteect ageteteegg tgte atg agg age tte aaa aga gte aac ttt Met Arg Ser Phe Lys Arg Val Asn Phe ggg act ctg cta agc agc cag aag gag gct gaa gag ttg ctg ccc gac 219 Gly Thr Leu Leu Ser Ser Gln Lys Glu Ala Glu Glu Leu Leu Pro Asp 10 ttg aag gag ttc ctg tcc aac cct cca gct ggt ttt ccc agc agc cga 267 Leu Lys Glu Phe Leu Ser Asn Pro Pro Ala Gly Phe Pro Ser Ser Arg tct gat gct gag agg aga caa gct tgt gat gcc atc ctg agg gct tgc 315 Ser Asp Ala Glu Arg Arg Gln Ala Cys Asp Ala Ile Leu Arg Ala Cys

aac cag cag ctg act gct aag cta gct tgc cct agg cat ctg ggg agc

363

Asn	Gln	Gln 60		Thr	Ala	Lys	Leu 65		Cys	Pro	Arg	His 70		Gly	Ser	
		Glu					Ala					Leu			acc Thr	411
	Gln					Tyr					Leu				ctg Leu 105	459
					Gln				gag Glu 115						Ala	507
									tgc Cys							555
									agc Ser							603
Gly	gca Ala 155	gaa Glu	gcc Ala	ctg Leu	ttg Leu	gaa Glu 160	cgg Arg	cga Arg	gct Ala	gca Ala	ttt Phe 165	gca Ala	gct Ala	cgg Arg	ctg Leu	651
aag Lys 170	gcc Ala	ttg Leu	agc Ser	ttc Phe	cta Leu 175	gta Val	ctc Leu	ttg Leu	gag Glu	gat Asp 180	gaa Glu	agt Ser	acc Thr	cct Pro	tgt Cys 185	699
gag Glu	gtt Val	cct Pro	cac His	ttt Phe 190	gct Ala	tct Ser	cca Pro	aca Thr	gcc Ala 195	tgt Cys	cga Arg	gcg Ala	gta Val	gct Ala 200	gcc Ala	747
cat His	cag Gln	cta Leu	ttt Phe 205	gat Asp	gcc Ala	agt Ser	ggc Gly	cat His 210	ggt Gly	cta Leu	aat Asn	gaa Glu	gca Ala 215	gat Asp	gct Ala	795
gat Asp	ttc Phe	cta Leu 220	gat Asp	gac Asp	ctg Leu	ctc Leu	tcc Ser 225	agg Arg	cac His	gtg Val	atc Ile	aga Arg 230	gcc Ala	ttg Leu	gtg Val	843
ggt Gly	gag Glu 235	aga Arg	Gly 393	agc Ser	tct Ser	tct Ser 240	gly ggg	ctt Leu	ctt Leu	tct Ser	ccc Pro 245	cag Gln	agg Arg	gcc Ala	ctc Leu	891
tgc Cys 250	ctc Leu	ttg Leu	gag Glu	ctc Leu	acc Thr 255	ttg Leu	gaa Glu	cac His	tgc Cys	cgt Arg 260	cgc Arg	ttt Phe	tgc Cys	tgg Trp	agc Ser 265	939
cgc Arg	cac His	cat His	gac Asp	aaa Lys 270	gcc Ala	atc Ile	agc Ser	gca Ala	gtg Val 275	gag Glu	aag Lys	gct Ala	cac His	agt Ser 280	tac Tyr	987
cta Leu	agg Arg	aac Asn	acc Thr 285	aat Asn	cta Leu	gcc Ala	Pro	agc Ser 290	ctt Leu	cag Gln	cta Leu	tgt Cys	cag Gln 295	ctg Leu	gly aaa	1035
gtt	aag	ctg	ctg	cag	gtt	999	gag	gaa	gga	cct	cag	gca	gtg	gcc	aag	1083

Val	Lys	Leu 300	Leu	Gln	Val	Gly	Glu 305		Gly	Pro	Gln	Ala 310	Val	Ala	Lys	
			_	_		_	_		_	_	-	Met		_	cca Pro	1131
	Pro	cca Pro													tca Ser 345	1179
		gaa Glu													ctg Leu	1227
		ttt Phe														1275
		gat Asp 380														1323
		atg Met														1371
Asp 410	Phe	gcc Ala	Gln	Gly	Cys 415	Gln	Ile	Val	Asp	Leu 420	Āla	Āsp	Leu	Thr	Gln 425	1419
Leu	Val	gac Asp	Ser	Cys 430	Lys	Ser	Thr	Val	Val 435	Trp	Met	Leu	Glu	Ala 440	Leu	1467
Glu	Gly	ctg Leu	Ser 445	Gly	Gln	Glu	Leu	Thr 450	Asp	His	Met	Gly	Met 455	Thr	Ala	1515
Ser	Tyr	acc Thr 460	Ser	Asn	Leu	Ala	Tyr 465	Ser	Phe	Tyr	Ser	His 470	Lys	Leu	Tyr	1563
Ala	Glu 475	gcc Ala	Cys	Ala	Ile	Ser 480	Glu	Pro	Leu	Cys	Gln 485	His	Leu	Gly	Leu	1611
Val 490	Lys	cca Pro	Gly	Thr	Tyr 495	Pro	Glu	Val	Pro	Pro 500	Glu	Lys	Leu	His	Arg 505	1659
Cys	Phe	cgg Arg	Leu	Gln 510	Val	Glu	Ser	Leu	Lys 515	Lys	Leu	Gly	Lys	Gln 520	Āla	1707
Gln	Gly		Lys 525	Met	Val	Ile	Leu	Trp 530	Leu	Ala	Ala	Leu	Gln 535	Pro	Cys	1755
agc Ser	cct Pro	gaa Glu	cac His	atg Met	gct Ala	gag Glu	cca Pro	gtc Val	act Thr	ttc Phe	tgg Trp	gtt Val	cgg Arg	gtc Val	aag Lys	1803

545 550 540 atg gat gcg gcc agg gct gga gac aag gag cta cag cta aag act ctg 1851 Met Asp Ala Ala Arg Ala Gly Asp Lys Glu Leu Gln Leu Lys Thr Leu cga gac agc ctc agt ggc tgg gac ccg gag acc ctg gcc ctc ctg ctg 1899 Arg Asp Ser Leu Ser Gly Trp Asp Pro Glu Thr Leu Ala Leu Leu Leu 575 580 agg gag gag ctg cag gcc tac aag gcg gtg cgg gcc gac act gga cag 1947 Arg Glu Glu Leu Gln Ala Tyr Lys Ala Val Arg Ala Asp Thr Gly Gln 595 gaa ege tte aac ate tgt gae ete etg gag etg age eec gag gag 1995 Glu Arg Phe Asn Ile Ile Cys Asp Leu Leu Glu Leu Ser Pro Glu Glu aca cca gcc ggg gcc tgg gca cga gcc acc cac ctg gta gaa ctg gct 2043 Thr Pro Ala Gly Ala Trp Ala Arg Ala Thr His Leu Val Glu Leu Ala 625 620 2091 cag gtg etc tgc tac cac gac ttt acg cag cag acc aac tgc tct gct Gln Val Leu Cys Tyr His Asp Phe Thr Gln Gln Thr Asn Cys Ser Ala 635 640 ctg gat gct atc cgg gaa gcc ctg cag ctt ctg gac tct gtg agg cct 2139 Leu Asp Ala Ile Arg Glu Ala Leu Gln Leu Leu Asp Ser Val Arg Pro 650 655 gag gcc cag gcc aga gat cag ctt ctg gac gat aaa gca cag gcc ttg 2187 Glu Ala Gln Ala Arg Asp Gln Leu Leu Asp Asp Lys Ala Gln Ala Leu 670 675 ctg tgg ctt tac atc tgt act ctg gaa gcc aaa ata cag gaa ggt atc 2235 Leu Trp Leu Tyr Ile Cys Thr Leu Glu Ala Lys Ile Gln Glu Gly Ile 685 690 695 gag cgg gat cgg aga gcc cag gcc cct ggt aac ttg gag gaa ttt gaa 2283 Glu Arg Asp Arg Arg Ala Gln Ala Pro Gly Asn Leu Glu Glu Phe Glu 700 705 gtc aat gac ctg aac tat gaa gat aaa ctc cag gaa gat cgt ttc cta 2331 Val Asn Asp Leu Asn Tyr Glu Asp Lys Leu Gln Glu Asp Arg Phe Leu 715 tac agt aac att gcc ttc aac ctg gct gca gat gct gct cag tcc aaa 2379 Tyr Ser Asn Ile Ala Phe Asn Leu Ala Ala Asp Ala Ala Gln Ser Lys 730 735 tgc ctg gac caa gcc ctg gcc ctg tgg aag gag ctg ctt aca aag ggg 2427 Cys Leu Asp Gln Ala Leu Ala Leu Trp Lys Glu Leu Leu Thr Lys Gly 750 2475 cag gcc cca gct gta cgg tgt ctc cag cag aca gcc tca ctg cag Gln Ala Pro Ala Val Arg Cys Leu Gln Gln Thr Ala Ala Ser Leu Gln

770

atc cta gca gcc ctc tac cag ctg gtg gca aag ccc atg cag gct ctg

775

2523

765

Ile	Leu	Ala 780	Ala	Leu	Tyr	Gln	Leu 785	Val	Ala	Lys	Pro	Met 790	Gln	Ala	Leu		
	_		ctg Leu	_				_			_	_	_	-		2571	
			gct Ala													2619	
			ccc Pro													2667	
			cat His 845													2715	
_		_	gat Asp	_		_	_							_	_	2763	
			ggt Gly													2811	
			tcc Ser										-			2859	
_	_		gca Ala	_			_		_							2907	
	-		gag Glu 925	-		_	_				_					2955	
			gac Asp													3003	
			gac Asp													3051	
			tat Tyr													3099	
			agc Ser										Gly			3147	
		Val	agt Ser 1005				Ala					Ala				3195	
aca	aca	aag	ctg	cag	ata	cca	cgc	cag	tgt	gcc	ctg	ttc	ctg	gtg	ctg	3243	

Thr Thr Lys Leu Gln Ile Pro Arg Gln Cys Ala Leu Phe Leu Val Leu 1020 1025 1030	
aag ggc gag ctg gag ctg gcc cgc aat gac att gat ctc tgt cag tcg Lys Gly Glu Leu Glu Leu Ala Arg Asn Asp Ile Asp Leu Cys Gln Ser 1035 1040 1045	3291
gac ctg cag cag gtt ctg ttc ttg ctt gag tct tgc aca gag ttt ggt Asp Leu Gln Gln Val Leu Phe Leu Leu Glu Ser Cys Thr Glu Phe Gly 1050 1055 1060 1065	3339
ggg gtg act cag cac ctg gac tct gtg aag aag gtc cac ctg cag aag Gly Val Thr Gln His Leu Asp Ser Val Lys Lys Val His Leu Gln Lys 1070 1075 1080	3387
ggg aag cag cag gcc cag gtc ccc tgt cct cca cag ctc cca gag gag Gly Lys Gln Gln Ala Gln Val Pro Cys Pro Pro Gln Leu Pro Glu Glu 1085 1090 1095	3435
gag ctc ttc cta aga ggc cct gct cta gag ctg gtg gcc act gtg gcc Glu Leu Phe Leu Arg Gly Pro Ala Leu Glu Leu Val Ala Thr Val Ala 1100 1105 1110	3483
aag gag cct ggc ccc ata gca cct tct aca aac tcc tcc cca gtc ttg Lys Glu Pro Gly Pro Ile Ala Pro Ser Thr Asn Ser Ser Pro Val Leu 1115 1120 1125	3531
aaa acc aag ccc cag ccc ata ccc aac ttc ctg tcc cat tca ccc acc Lys Thr Lys Pro Gln Pro Ile Pro Asn Phe Leu Ser His Ser Pro Thr 1130 1135 1140 1145	3579
tgt gac tgc tcg ctc tgc gcc agc cct gtc ctc aca gca gtc tgt ctg Cys Asp Cys Ser Leu Cys Ala Ser Pro Val Leu Thr Ala Val Cys Leu 1150 1155 1160	3627
cgc tgg gta ttg gtc acg gca ggg gtg agg ctg gcc atg ggc cac caa Arg Trp Val Leu Val Thr Ala Gly Val Arg Leu Ala Met Gly His Gln 1165 1170 1175	3675
gcc cag ggt ctg gat ctg ctg cag gtc gtg ctg aag ggc tgt cct gaa Ala Gln Gly Leu Asp Leu Leu Gln Val Val Leu Lys Gly Cys Pro Glu 1180 1185 1190	3723
gcc gct gag cgc ctc acc caa gct ctc caa gct tcc ctg aat cat aaa Ala Ala Glu Arg Leu Thr Gln Ala Leu Gln Ala Ser Leu Asn His Lys 1195 1200 1205	3771
aca ccc ccc tcc ttg gtt cca agc ctc ttg gat gag atc ttg gct caa Thr Pro Pro Ser Leu Val Pro Ser Leu Leu Asp Glu Ile Leu Ala Gln 1210 1215 1220 1225	3819
gca tac aca ctg ttg gca ctg gag ggc ctg aac cag cca tca aac gag Ala Tyr Thr Leu Leu Ala Leu Glu Gly Leu Asn Gln Pro Ser Asn Glu 1230 1235 1240	3867
agc ctg cag aag gtt cta cag tca ggg ctg aag ttt gta gca gca cgg Ser Leu Gln Lys Val Leu Gln Ser Gly Leu Lys Phe Val Ala Ala Arg 1245 1250 1255	3915
ata ccc cac cta gag ccc tgg cga gcc agc ctg ctc ttg att tgg gcc	3963

Ile Pro	His 1260	Leu	Glu	Pro		Arg 1265	Ala	Ser	Leu		Leu 1270	Ile	Trp	Ala	
ctc aca Leu Thr 1275				Gly					Thr						4011
agc tcc Ser Ser 1290			Trp	_				Ile		_	_		Gly		4059
gag ccc Glu Pro		Lys		_			Lys	_				Gly			4107
aag tta Lys Leu	Ala					Ser					Ser				4155
ctg gaa Leu Glu					Pro					Pro					4203
agg caa Arg Gln 1355				His					Val						4251
cct aca Pro Thr 1370			Lys					Gln					Gln		4299
aga gtc Arg Val		Thr					Asn					Ser			4347
gaa gac Glu Asp	Pro					Āla					Glu				4395
cgg ggc Arg Gly					Gly					Arg					4443
cta aag Leu Lys 1435				Val					Ser						4491
ggc ctg Gly Leu 1450			Arg					Lys					Arg		4539
tgt gag Cys Glu		Arg					Āla					Arg			4587
cct gag Pro Glu	Ile					Pro					Thr				4635
aga aaa	atg	agc	ttt	gag	atc	ctc	agg	ggc	tct	gac	999	gaa	gac	tca	4683

Arg Lys Met Ser 1500	Phe Glu Ile Le		sp Gly Glu Asp Ser 1510
	_	a Pro Gly Pro G	ag gca gct tct gga 4731 lu Ala Ala Ser Gly 25
			ag aag ctg ccc agc 4779 ys Lys Leu Pro Ser 1545
Pro Cys Pro Asp			gt cct cgg ctc cag 4827 ly Pro Arg Leu Gln 1560
_			cc ctg gac tcc atc 4875 hr Leu Asp Ser Ile 1575
		e Arg Gly Ile S	gt cac tgt cct cct 4923 er His Cys Pro Pro 1590
		s Arg Phe Leu A	cc ttg tgc ctg ggc 4971 la Leu Cys Leu Gly 05
			cc gag tct gtc tcc 5019 hr Glu Ser Val Ser 1625
Ile Thr Cys Arg			ac aga cag ctc agc 5067 is Arg Gln Leu Ser 1640
			ca gac cag ctg cag 5115 la Asp Gln Leu Gln 1655
		o Gly Asp Val P	cc ctg gcc cgc atc 5163 ro Leu Ala Arg Ile 1670
		a Leu Glu Ser G	gc cac ttc ccc cag 5211 ly His Phe Pro Gln 85
			tg atc ccc agt ggg 5259 eu Ile Pro Ser Gly 1705
Val Thr Val Cys			ag ccc gga acc gtg 5307 ln Pro Gly Thr Val 1720
ggc aac acc ctc Gly Asn Thr Leu 1725			ac agt ccc cca gtc 5355 sp Ser Pro Pro Val
	bed bed int At	1730	1735

Ser Val Gln Ile P 1740	ro Thr Gly Glr 1745		is Leu Arg Ser Val 1750
		Lys Ala Gln L	aa gag aac agc agc 5451 ys Glu Asn Ser Ser 65
			tg gca ctg gac cac 5499 eu Ala Leu Asp His 1785
Arg Met Glu Val L			ct gtg ctg ggc tgc 5547 er Val Leu Gly Cys 1800
			cc ggc cct gcc cag 5595 ro Gly Pro Ala Gln 1815
		Leu Gln Asp C	gt ggc tgg aaa tat 5643 ys Gly Trp Lys Tyr 1830
		Met Leu Ser G	gt gcc ggt gcc ctc 5691 ly Ala Gly Ala Leu 45
			tg tgc cca acc cag 5739 eu Cys Pro Thr Gln 1865
Pro Glu Arg Ala G			ta gga cgt cta cag 5787 al Gly Arg Leu Gln 1880
			tg gtc cta gac aag 5835 eu Val Leu Asp Lys 1895
		Ser Met Pro S	gc ctc caa gca ctg 5883 er Leu Gln Ala Leu 1910
	_	_	tc agc tac tcc atc 5931 eu Ser Tyr Ser Ile 25
			aa ggg gtg gat cca 5979 ln Gly Val Asp Pro 1945
	yr Val Leu Asn		ac ctg tca agc aca 6027 sn Leu Ser Ser Thr 1960
			ct ggc tgg aga gga 6075 la Gly Trp Arg Gly 1975
gtg gtt ggg gag g	tg cca aga cct	gaa cag gtg c	ag gaa gcc ctg aca 6123

Val Val Gly Glu Val Pro Arg Pro Glu Gln Val Gln Glu Ala Leu Thr 1980 1985 1990
aag cat gat ttg tat atc tat gca ggg cat ggg gct ggt gcc cgc ttc 6171 Lys His Asp Leu Tyr Ile Tyr Ala Gly His Gly Ala Gly Ala Arg Phe 1995 2000 2005
ctt gat ggg cag gct gtc ctg cgg ctg agc tgt cgg gca gtg gcc ctg Leu Asp Gly Gln Ala Val Leu Arg Leu Ser Cys Arg Ala Val Ala Leu 2010 2015 2020 2025
ctg ttt ggc tgt agc agt gcg gcc ctg gct gtg cat gga aac ctg gag 6267 Leu Phe Gly Cys Ser Ser Ala Ala Leu Ala Val His Gly Asn Leu Glu 2030 2035 2040
ggg gct ggc atc gtg ctc aag tac atc atg gct ggt tgc ccc ttg ttt Gly Ala Gly Ile Val Leu Lys Tyr Ile Met Ala Gly Cys Pro Leu Phe 2045 2050 2055
ctg ggt aat ctc tgg gat gtg act gac cgc gac att gac cgc tac acg 6363 Leu Gly Asn Leu Trp Asp Val Thr Asp Arg Asp Ile Asp Arg Tyr Thr 2060 2065 2070
gaa get etg etg eaa gge tgg ett gga gea gge eea ggg gee eec ett 6411 Glu Ala Leu Leu Gln Gly Trp Leu Gly Ala Gly Pro Gly Ala Pro Leu 2075 2080 2085
ctc tac tat gta aac cag gcc cgc caa gct ccc cga ctc aag tat ctt 6459 Leu Tyr Tyr Val Asn Gln Ala Arg Gln Ala Pro Arg Leu Lys Tyr Leu 2090 2095 2100 2105
att ggg gct gca cct ata gcc tat ggc ttg cct gtc tct ctg cgg taa 6507 Ile Gly Ala Ala Pro Ile Ala Tyr Gly Leu Pro Val Ser Leu Arg 2110 2115 2120
ccccatggag ctgtcttatt gatgctagaa gcctcataac tgttctacct ccaaggttag 6567
atttaatcct taggataact cttttaaagt gattttcccc agtgttttat atgaaacatt 6627
tccttttgat ttaacctcag tataataaag atacatcatt t
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Lys Glu Ala Glu Glu Leu Leu Pro Asp Leu Lys Glu Phe Leu Ser Asn 20 25 30
Pro Pro Ala Gly Phe Pro Ser Ser Arg Ser Asp Ala Glu Arg Arg Gln 35 40 45
Ala Cys Asp Ala Ile Leu Arg Ala Cys Asn Gln Gln Leu Thr Ala Lys 50 55 60

Leu Ala Cys Pro Arg His Leu Gly Ser Leu Leu Glu Leu Ala Glu Leu Ala Cys Asp Gly Tyr Leu Val Ser Thr Pro Gln Arg Pro Pro Leu Tyr Leu Glu Arg Ile Leu Phe Val Leu Leu Arg Asn Ala Ala Gln Gly 100 Ser Pro Glu Val Thr Leu Arg Leu Ala Gln Pro Leu His Ala Cys Leu 120 Val Gln Cys Ser Arg Glu Ala Ala Pro Gln Asp Tyr Glu Ala Val Ala 130 135 Arg Gly Ser Phe Ser Leu Leu Trp Lys Gly Ala Glu Ala Leu Leu Glu Arg Arg Ala Ala Phe Ala Ala Arg Leu Lys Ala Leu Ser Phe Leu Val Leu Leu Glu Asp Glu Ser Thr Pro Cys Glu Val Pro His Phe Ala Ser Pro Thr Ala Cys Arg Ala Val Ala Ala His Gln Leu Phe Asp Ala Ser Gly His Gly Leu Asn Glu Ala Asp Ala Asp Phe Leu Asp Asp Leu Leu 210 Ser Arg His Val Ile Arg Ala Leu Val Gly Glu Arg Gly Ser Ser Ser 230 Gly Leu Leu Ser Pro Gln Arg Ala Leu Cys Leu Leu Glu Leu Thr Leu 250 245 Glu His Cys Arg Arg Phe Cys Trp Ser Arg His His Asp Lys Ala Ile Ser Ala Val Glu Lys Ala His Ser Tyr Leu Arg Asn Thr Asn Leu Ala 275 280 Pro Ser Leu Gln Leu Cys Gln Leu Gly Val Lys Leu Leu Gln Val Gly Glu Glu Gly Pro Gln Ala Val Ala Lys Leu Leu Ile Lys Ala Ser Ala 305 310 315 320 Val Leu Ser Lys Ser Met Glu Ala Pro Ser Pro Pro Leu Arg Ala Leu 330 Tyr Glu Ser Cys Gln Phe Phe Leu Ser Gly Leu Glu Arg Gly Thr Lys Arg Arg Tyr Arg Leu Asp Ala Ile Leu Ser Leu Phe Ala Phe Leu Gly Gly Tyr Cys Ser Leu Leu Gln Gln Leu Arg Asp Asp Gly Val Tyr Gly 375 380

Gly Ser Ser Lys Gln Gln Gln Ser Phe Leu Gln Met Tyr Phe Gln Gly 390 395 Leu His Leu Tyr Thr Val Val Tyr Asp Phe Ala Gln Gly Cys Gln 405 410 Ile Val Asp Leu Ala Asp Leu Thr Gln Leu Val Asp Ser Cys Lys Ser 425 420 Thr Val Val Trp Met Leu Glu Ala Leu Glu Gly Leu Ser Gly Gln Glu 440 Leu Thr Asp His Met Gly Met Thr Ala Ser Tyr Thr Ser Asn Leu Ala 450 Tyr Ser Phe Tyr Ser His Lys Leu Tyr Ala Glu Ala Cys Ala Ile Ser 470 475 Glu Pro Leu Cys Gln His Leu Gly Leu Val Lys Pro Gly Thr Tyr Pro Glu Val Pro Pro Glu Lys Leu His Arg Cys Phe Arg Leu Gln Val Glu Ser Leu Lys Lys Leu Gly Lys Gln Ala Gln Gly Cys Lys Met Val Ile Leu Trp Leu Ala Ala Leu Gln Pro Cys Ser Pro Glu His Met Ala Glu 530 Pro Val Thr Phe Trp Val Arg Val Lys Met Asp Ala Ala Arg Ala Gly 550 Asp Lys Glu Leu Gln Leu Lys Thr Leu Arg Asp Ser Leu Ser Gly Trp 570 Asp Pro Glu Thr Leu Ala Leu Leu Arg Glu Glu Leu Gln Ala Tyr Lys Ala Val Arg Ala Asp Thr Gly Gln Glu Arg Phe Asn Ile Ile Cys 595 600 Asp Leu Leu Glu Leu Ser Pro Glu Glu Thr Pro Ala Gly Ala Trp Ala 615 Arg Ala Thr His Leu Val Glu Leu Ala Gln Val Leu Cys Tyr His Asp 625 630 Phe Thr Gln Gln Thr Asn Cys Ser Ala Leu Asp Ala Ile Arg Glu Ala 645 650 Leu Gln Leu Leu Asp Ser Val Arg Pro Glu Ala Gln Ala Arg Asp Gln 660 665 Leu Leu Asp Asp Lys Ala Gln Ala Leu Leu Trp Leu Tyr Ile Cys Thr 680 Leu Glu Ala Lys Ile Gln Glu Gly Ile Glu Arg Asp Arg Arg Ala Gln 700

Ala Pro Gly Asn Leu Glu Glu Phe Glu Val Asn Asp Leu Asn Tyr Glu 715 710 Asp Lys Leu Gln Glu Asp Arg Phe Leu Tyr Ser Asn Ile Ala Phe Asn Leu Ala Ala Asp Ala Ala Gln Ser Lys Cys Leu Asp Gln Ala Leu Ala Leu Trp Lys Glu Leu Leu Thr Lys Gly Gln Ala Pro Ala Val Arg Cys Leu Gln Gln Thr Ala Ala Ser Leu Gln Ile Leu Ala Ala Leu Tyr Gln 770 775 Leu Val Ala Lys Pro Met Gln Ala Leu Glu Val Leu Leu Leu Arg 790 795 Ile Val Ser Glu Arg Leu Lys Asp His Ser Lys Ala Ala Gly Ser Ser Cys His Ile Thr Gln Leu Leu Thr Leu Gly Cys Pro Ser Tyr Ala Gln Leu His Leu Glu Glu Ala Ala Ser Ser Leu Lys His Leu Asp Gln Thr Thr Asp Thr Tyr Leu Leu Ser Leu Thr Cys Asp Leu Leu Arg 850 Ser Gln Leu Tyr Trp Thr His Gln Lys Val Thr Lys Gly Val Ser Leu 870 Leu Leu Ser Val Leu Arg Asp Pro Ala Leu Gln Lys Ser Ser Lys Ala Trp Tyr Leu Leu Arg Val Gln Val Leu Gln Leu Val Ala Ala Tyr Leu 905 Ser Leu Pro Ser Asn Asn Leu Ser His Ser Leu Trp Glu Gln Leu Cys 915 920 Ala Gln Gly Trp Gln Thr Pro Glu Ile Ala Leu Ile Asp Ser His Lys 935 Leu Leu Arg Ser Ile Ile Leu Leu Met Gly Ser Asp Ile Leu Ser 945 950 955 Thr Gln Lys Ala Ala Val Glu Thr Ser Phe Leu Asp Tyr Gly Glu Asn 970 Leu Val Gln Lys Trp Gln Val Leu Ser Glu Val Leu Ser Cys Ser Glu 980 985 990 Lys Leu Val Cys His Leu Gly Arg Leu Gly Ser Val Ser Glu Ala Lys 1000 Ala Phe Cys Leu Glu Ala Leu Lys Leu Thr Thr Lys Leu Gln Ile Pro 1015

- Arg Gln Cys Ala Leu Phe Leu Val Leu Lys Gly Glu Leu Glu Leu Ala 1025 1030 1035 1040
- Arg Asn Asp Ile Asp Leu Cys Gln Ser Asp Leu Gln Gln Val Leu Phe
 1045 1050 1055
- Leu Leu Glu Ser Cys Thr Glu Phe Gly Gly Val Thr Gln His Leu Asp 1060 1065 1070
- Ser Val Lys Lys Val His Leu Gln Lys Gly Lys Gln Gln Ala Gln Val 1075 1080 1085
- Pro Cys Pro Pro Gln Leu Pro Glu Glu Leu Phe Leu Arg Gly Pro 1090 1095 1100
- Ala Leu Glu Leu Val Ala Thr Val Ala Lys Glu Pro Gly Pro Ile Ala 1105 1110 1115 1120
- Pro Ser Thr Asn Ser Ser Pro Val Leu Lys Thr Lys Pro Gln Pro Ile 1125 1130 1135
- Pro Asn Phe Leu Ser His Ser Pro Thr Cys Asp Cys Ser Leu Cys Ala 1140 1145 1150
- Ser Pro Val Leu Thr Ala Val Cys Leu Arg Trp Val Leu Val Thr Ala 1155 1160 1165
- Gly Val Arg Leu Ala Met Gly His Gln Ala Gln Gly Leu Asp Leu Leu 1170 1180
- Gln Val Val Leu Lys Gly Cys Pro Glu Ala Ala Glu Arg Leu Thr Gln 1185 1190 1195 1200
- Ala Leu Gln Ala Ser Leu Asn His Lys Thr Pro Pro Ser Leu Val Pro 1205 1210 1215
- Ser Leu Leu Asp Glu Ile Leu Ala Gln Ala Tyr Thr Leu Leu Ala Leu 1220 1225 1230
- Glu Gly Leu Asn Gln Pro Ser Asn Glu Ser Leu Gln Lys Val Leu Gln 1235 1240 1245
- Ser Gly Leu Lys Phe Val Ala Ala Arg Ile Pro His Leu Glu Pro Trp 1250 1255 1260
- Arg Ala Ser Leu Leu Leu Ile Trp Ala Leu Thr Lys Leu Gly Gly Leu 1265 1270 1275 1280
- Ser Cys Cys Thr Thr Gln Leu Phe Ala Ser Ser Trp Gly Trp Gln Pro 1285 1290 1295
- Pro Leu Ile Lys Ser Val Pro Gly Ser Glu Pro Ser Lys Thr Gln Gly 1300 1305 1310
- Gln Lys Arg Ser Gly Arg Gly Arg Gln Lys Leu Ala Ser Ala Pro Leu 1315 1320 1325
- Ser Leu Asn Asn Thr Ser Gln Lys Gly Leu Glu Gly Arg Gly Leu Pro 1330 1335 1340

- Cys Thr Pro Lys Pro Pro Asp Arg Ile Arg Gln Ala Gly Pro His Val 1345 1350 1355 1360
- Pro Phe Thr Val Phe Glu Glu Val Cys Pro Thr Glu Ser Lys Pro Glu 1365 1370 1375
- Val Pro Gln Ala Pro Arg Val Gln Gln Arg Val Gln Thr Arg Leu Lys 1380 1385 1390
- Val Asn Phe Ser Asp Asp Ser Asp Leu Glu Asp Pro Val Ser Ala Glu 1395 1400 1405
- Ala Trp Leu Ala Glu Glu Pro Lys Arg Gly Thr Ala Ser Arg Gly 1410 1415 1420
- Arg Gly Arg Ala Arg Lys Gly Leu Ser Leu Lys Thr Asp Ala Val Val 1425 1430 1435 1440
- Ala Pro Gly Ser Ala Pro Gly Asn Pro Gly Leu Asn Gly Arg Ser Arg 1445 1450 1455
- Arg Ala Lys Lys Val Ala Ser Arg His Cys Glu Glu Arg Arg Pro Gln
 1460 1465 1470
- Arg Ala Ser Asp Gln Ala Arg Pro Gly Pro Glu Ile Met Arg Thr Ile 1475 1480 1485
- Pro Glu Glu Glu Leu Thr Asp Asn Trp Arg Lys Met Ser Phe Glu Ile 1490 1495 1500
- Leu Arg Gly Ser Asp Gly Glu Asp Ser Ala Ser Gly Gly Lys Thr Pro 1505 1510 1515 1520
- Ala Pro Gly Pro Glu Ala Ala Ser Gly Glu Trp Glu Leu Leu Arg Leu 1525 1530 1535
- Asp Ser Ser Lys Lys Leu Pro Ser Pro Cys Pro Asp Lys Glu Ser 1540 1545 1550
- Asp Lys Asp Leu Gly Pro Arg Leu Gln Leu Pro Ser Ala Pro Val Ala 1555 1560 1565
- Thr Gly Leu Ser Thr Leu Asp Ser Ile Cys Asp Ser Leu Ser Val Ala 1570 1575 1580
- Phe Arg Gly Ile Ser His Cys Pro Pro Ser Gly Leu Tyr Ala His Leu 1585 1590 1595 1600
- Cys Arg Phe Leu Ala Leu Cys Leu Gly His Arg Asp Pro Tyr Ala Thr 1605 1610 1615
- Ala Phe Leu Val Thr Glu Ser Val Ser Ile Thr Cys Arg His Gln Leu 1620 1625 1630
- Leu Thr His Leu His Arg Gln Leu Ser Lys Ala Gln Lys His Arg Gly 1635 1640 1645
- Ser Leu Glu Ile Ala Asp Gln Leu Gln Gly Leu Ser Leu Gln Glu Met 1650 1655 1660
- Pro Gly Asp Val Pro Leu Ala Arg Ile Gln Arg Leu Phe Ser Phe Arg

1665 1670 1675 1680 Ala Leu Glu Ser Gly His Phe Pro Gln Pro Glu Lys Glu Ser Phe Gln 1685 1690 Glu Arg Leu Ala Leu Ile Pro Ser Gly Val Thr Val Cys Val Leu Ala 1705 Leu Ala Thr Leu Gln Pro Gly Thr Val Gly Asn Thr Leu Leu Leu Thr 1715 1720 Arg Leu Glu Lys Asp Ser Pro Pro Val Ser Val Gln Ile Pro Thr Gly 1735 Gln Asn Lys Leu His Leu Arg Ser Val Leu Asn Glu Phe Asp Ala Ile 1750 1755 Gln Lys Ala Gln Lys Glu Asn Ser Ser Cys Thr Asp Lys Arg Glu Trp Trp Thr Gly Arg Leu Ala Leu Asp His Arg Met Glu Val Leu Ile Ala 1785 Ser Leu Glu Lys Ser Val Leu Gly Cys Trp Lys Gly Leu Leu Pro 1795 1800 Ser Ser Glu Glu Pro Gly Pro Ala Gln Glu Ala Ser Arg Leu Gln Glu 1815 Leu Leu Gln Asp Cys Gly Trp Lys Tyr Pro Asp Arg Thr Leu Leu Lys 1825 1830 1835 1840 Ile Met Leu Ser Gly Ala Gly Ala Leu Thr Pro Gln Asp Ile Gln Ala 1845 1850 Leu Ala Tyr Gly Leu Cys Pro Thr Gln Pro Glu Arg Ala Gln Glu Leu 1860 1865 Leu Asn Glu Ala Val Gly Arg Leu Gln Gly Leu Thr Val Pro Ser Asn 1880 Ser His Leu Val Leu Val Leu Asp Lys Asp Leu Gln Lys Leu Pro Trp 1890 1895 1900 Glu Ser Met Pro Ser Leu Gln Ala Leu Pro Val Thr Arg Leu Pro Ser Phe Arg Phe Leu Leu Ser Tyr Ser Ile Ile Lys Glu Tyr Gly Ala Ser Pro Val Leu Ser Gln Gly Val Asp Pro Arg Ser Thr Phe Tyr Val Leu Asn Pro His Asn Asn Leu Ser Ser Thr Glu Glu Gln Phe Arg Ala Asn 1960 Phe Ser Ser Glu Ala Gly Trp Arg Gly Val Val Gly Glu Val Pro Arg 1970

Pro Glu Gln Val Gln Glu Ala Leu Thr Lys His Asp Leu Tyr Ile Tyr

1985 1990 1995 2000 Ala Gly His Gly Ala Gly Ala Arg Phe Leu Asp Gly Gln Ala Val Leu 2010 Arg Leu Ser Cys Arg Ala Val Ala Leu Leu Phe Gly Cys Ser Ser Ala Ala Leu Ala Val His Gly Asn Leu Glu Gly Ala Gly Ile Val Leu Lys 2040 Tyr Ile Met Ala Gly Cys Pro Leu Phe Leu Gly Asn Leu Trp Asp Val 2055 Thr Asp Arg Asp Ile Asp Arg Tyr Thr Glu Ala Leu Leu Gln Gly Trp 2065 2070 Leu Gly Ala Gly Pro Gly Ala Pro Leu Leu Tyr Tyr Val Asn Gln Ala 2085 2090 Arg Gln Ala Pro Arg Leu Lys Tyr Leu Ile Gly Ala Ala Pro Ile Ala 2100 2105 Tyr Gly Leu Pro Val Ser Leu Arg <210> 3 <211> 33 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: primer ggccaattga tatcatgagg agcttcaaaa gag 33 <210> 4 <211> 24 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: primer 24 caactgtcca ctagttgggt cagg <210> 5 <211> 54 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: primer

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